



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/922,067D
Source: 1600
Date Processed by STIC: 10/2/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mallroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>09/922,067D</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.	
11 <input checked="" type="checkbox"/> Use of <220>	Sequence(s) <u>5-7</u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/922,067D

DATE: 10/02/2003

TIME: 15:54:11

Input Set : A:\p30693c4x1c1seqlist.txt

Output Set: N:\CRF4\10022003\I922067D.raw

4 <110> APPLICANT: MacPhee, Colin Houston
5 Tew, David Graham
6 Southan, Christopher Donald
7 Hickey, Deirdre Mary Bernadette
8 Gloger, Israel Simon
9 Lawrence, Geoffrey Mark Prouse
10 Rice, Simon Quentyn John
12 <120> TITLE OF INVENTION: Lipoprotein Associated Phospholipase A2,
13 Inhibitors Thereof and Use of the Same in Diagnosis and
14 Therapy
16 <130> FILE REFERENCE: P30693C4X1C1
18 <140> CURRENT APPLICATION NUMBER: 09/922,067D
19 <141> CURRENT FILING DATE: 2001-08-03
21 <150> PRIOR APPLICATION NUMBER: 09/193,130
22 <151> PRIOR FILING DATE: 2000-11-28
24 <150> PRIOR APPLICATION NUMBER: 08/387,858
25 <151> PRIOR FILING DATE: 1994-06-24
27 <150> PRIOR APPLICATION NUMBER: PCT/GB94/01374
28 <151> PRIOR FILING DATE: 1994-06-24
30 <150> PRIOR APPLICATION NUMBER: GB 9313144.9
31 <151> PRIOR FILING DATE: 1993-06-25
E--> 33 <160> NUMBER OF SEQ ID NOS: 11 13 (see below)
35 <170> SOFTWARE: FastSEQ for Windows Version 4.0

Does Not
Corrected Draft

[Handwritten signature]

Does Not Comply
Corrected Diskette Needed

pp 1-2

ERRORED SEQUENCES

309 <210> SEQ ID NO: 12
310 <211> LENGTH: 7
311 <212> TYPE: PRT
312 <213> ORGANISM: Homo sapien
E--> 314 <400> SEQUENCE: (10) 12 ← large to
315 Gln Tyr Ile Asn Pro Ala Val
316 1 5
319 <210> SEQ ID NO: 13
320 <211> LENGTH: 5
321 <212> TYPE: PRT
322 <213> ORGANISM: Homo sapien
E--> 324 <400> SEQUENCE: (10) 13
325 Gln Tyr Ile Asn Pro
326 1 5
330 (6/6) delete
last sequence in submitted file

09/923,0670 Z

<210> 5
<211> 420
<212> DNA
<213> Unknown

needs explanation (see item 11 on Error Summary Sheet)

<220>
<221> misc_feature
<222> 265, 390, 395, 403, 406
<223> n = A, T, C or G

<400> 5
aaaaaaccta ttttaatcct aattgtatct ctctattcct gaagagttct gtaacatgat 60
gtgttgattg gttgtgttaa tgttggtccc tggaataaga ttctcatcat ctcttcaat 120
caagcagtc cactgatcaa aatctttatg aagtcctaaa tgcttttgta agaattgctaa 180
tgaagctttg ttgctaagat caatagctgc atttgaatct atgtctccct ttaatttgag 240
catgtgtcca attattttgc cagtngcaaa agtgaagtca gcaaaattct ggtggactga 300
acccttgatt gtaatcatct ttctttcttt atcaggtgag tagcattttt tcatttttat 360
gatattagca ggatattgga aatattcagn gttgntaaaa agngngngct gagggattct 420

<210> 6
<211> 379
<212> DNA
<213> Unknown

same error

<220>
<221> misc_feature
<222> 84
<223> n = A, T, C or G

<400> 6
tgctaataatc ataaaaatga aaaaatgcta ctcacctgat aaagaaagaa agatgattac 60
aatcaggggt tcagtcacc aganttttgc tgacttcact tttgcaactg gcaaaataat 120
tggacacatg ctcaaattaa agggagacat agattcaaat gtagctattg atcttagcaa 180
caaagcttca ttagcattct taaaaagca tttaggactt cataaagatt ttgttcagt 240
ggactgcttg attgaaggag atgatgagaa tcttattcca gggaccaaca ttaacacaac 300
caattcaaca catcatgttt acagaacttc ttccagggaa taggaggaaa tacaattggg 360
gtttaaaata ggttttttt 379

<210> 7
<211> 279
<212> DNA
<213> Unknown

same

<220>
<221> misc_feature
<222> 257
<223> n = A, T, C or G

<400> 7
gaagaatgca ttagatttaa agtttgatat ggaacaactg aaggactota ttgataggga 60
aaaaatagca gtaattggac attcttttgg tggagcaacg gttattcaga ctcttagtga 120
agatcagaga ttcagatgtg gtattgccct ggatgcattg atgtttccac tgggtgatga 180
agtatattcc agaattcctc agccctctt ttttatcaac tctgaatatt tccaatatcc 240
tgctaataatc ataaaantgg aaaaatgcta ctcacctgg 279

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/922,067D

DATE: 10/02/2003

TIME: 15:54:12

Input Set : A:\p30693c4x1c1seqlist.txt

Output Set: N:\CRF4\10022003\I922067D.raw

L:102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:240

M:341 Repeated in SeqNo=5

L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:60

L:141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:240

L:314 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:12 differs:10

L:324 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:13 differs:10

L:33 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (11) Counted (13)